<table>
<thead>
<tr>
<th>Title</th>
<th>Automated Creation of Beamformer-Based Optimum DOA Estimation Algorithm Using Genetic Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Yoshimura, Shunsuke; Hirayama, Hiroshi; Kikuma, Nobuyoshi; Sakakibara, Kunio</td>
</tr>
<tr>
<td>Citation</td>
<td>IEICE transactions on communications, E95B(10): 3332-3336</td>
</tr>
<tr>
<td>Issue Date</td>
<td>2012-10-00</td>
</tr>
<tr>
<td>URL</td>
<td><a href="http://repo.lib.nitech.ac.jp/handle/123456789/24096">http://repo.lib.nitech.ac.jp/handle/123456789/24096</a></td>
</tr>
<tr>
<td>Rights</td>
<td>(c) 2012 The Institute of Electronics, Information and Communication Engineers</td>
</tr>
<tr>
<td>Type</td>
<td>Journal Article</td>
</tr>
<tr>
<td>Textversion</td>
<td>publisher</td>
</tr>
</tbody>
</table>

名古屋工業大学学術機関リポジトリ
Nagoya Institute of Technology Repository
http://repo.lib.nitech.ac.jp

・名古屋工業大学学術機関リポジトリは、名古屋工業大学内で生産された学術情報を電子的に収集・保存・発信するシステムです。
・論文の著作権は、著者または出版社が保持しています。著作権法で定める権利制限規定を超える利用については、著作権者に許諾を得てください。
・文書の「Author」と記載された論文は、著者原稿となります。実際の出版社版とは、レイアウト、字句校正レベルの異同がある場合もあります。

・名古屋工業大学学術機関リポジトリでは、著作権法で定める権利制限規定を超える利用については、著作権者に許諾を必要とします。
・文書の「Author」と記載された論文は、著者原稿となります。実際の出版社版とは、レイアウト、字句校正レベルの異同がある場合もあります。

Nagoya Institute of Technology Repository System is built to collect, archive and offer electronically the academic information produced by Nagoya Institute of Technology.
The copyright and related rights of the article are held by authors or publishers.
The copyright owners' consents must be required to use it over the curtailment of copyrights.
・Textversion "Author " means the article is author's version.
Author version may have some difference in layouts and wordings form publisher version.
LETTER

Automated Creation of Beamformer-Based Optimum DOA Estimation Algorithm Using Genetic Algorithm

Shunsuke YOSHIMURA†, Nonmember, Hiroshi HIRAYAMA†(a), Member, Nobuyoshi KIKUMA†, Fellow, and Kunio SAKAKIBARA†, Senior Member

SUMMARY A novel method for automatically creating an optimum direction-of-arrival (DOA) estimation algorithm for a given radio environment using a genetic algorithm (GA) is proposed. DOA estimation algorithms are generally described by parameters and operators. The performance of a DOA estimation algorithm is evaluated using root mean square error (RMSE) through computer simulations. A GA searches for the combination of parameters and operators that gives the lowest RMSE. Because a GA can treat only bit strings, Polish notation is used to convert bit strings into a DOA estimation algorithm. A computer simulation showed that the proposed method can create a new angle spectrum function. The created angle spectrum function has higher resolution than the Capon method.

key words: array antenna, DOA estimation, genetic algorithm, genetic programming, Polish notation, combinatorial optimization

1. Introduction

Direction-of-arrival (DOA) estimation technology using an array antenna has many applications such as location of wireless terminals, vehicle radar, and so on. Various DOA estimation algorithms have been proposed [1]. Each algorithm has advantages and disadvantages while individual applications have specific requirements such as low signal-to-noise ratio (SNR), small number of snapshots, high correlation among incoming waves, and low calculation cost. Therefore, it is necessary to properly use algorithms according to each requirement. To meet individual requirements, trial-and-error investigations by using computer simulation have been conducted.

On the other hand, significant developments in computer capability have enabled the development of repetition type optimization algorithms. A genetic algorithm (GA) is a powerful meta-heuristic repetition-type optimization algorithm, especially for combinatorial optimization problems [2]. When fitness is calculated from bit strings (which is called a chromosome in a GA), the GA finds the chromosome that minimize fitness. By adopting chromosomes to individual applications, a GA is applicable for any kind of combinatorial optimization problem. For example, an algorithm is optimized using a GA through tree-structure expression with Polish notation, which is known as genetic programming (GP) [3].

In antenna engineering, the design of an antenna structure using a GA has been proposed [4]–[6]. A GA was used to create an equivalent circuit [7]. A DOA estimation algorithm using a GA was also proposed [8], [9]. However, using a GA to create an optimum DOA estimation algorithm has not been proposed. We propose a method for creating optimum DOA estimation algorithms by using a GA. In Sect. 2, proposed procedure is described. In Sect. 3, proposed procedure is numerically evaluated. We conclude the paper in Sect. 4.

2. Proposed Method

2.1 Overview of Proposed Method

The proposed method consists of three steps: 1) A GA optimizes bit strings with respect to their fitness, 2) bit strings are transformed into angle spectrum functions by using Polish notation, and 3) DOA estimation simulation is conducted by using the angle spectrum functions to evaluate their performances as fitness. This procedure is shown in Fig. 1. By repeating this procedure, angle spectrum functions with good root mean square error (RMSE) can survive and a better angle spectrum function is created.

2.2 Transformation from Chromosomes into Angle Spectrum Function

A GA optimizes chromosomes, which consist of several genes. In the proposed method, genes correspond to parameters and operators, and a chromosome corresponds to an angle spectrum function.

Table 1 lists the assignment of genes to parameters and
operators. A gene consists of 3 bits; therefore one gene represents $2^3 = 8$ kinds of parameters and operators. Genes are described in decimal expression in this table. Genes 2, 3, and 6 are parameters and 0, 1, 4, and 5 are operators. Gene 7 is blank.

Polish notation is an expression of a numerical formula for putting operators before operands (parameters). By using Polish notation, any numerical formula is expressed without using parentheses. In the proposed method, the Polish notation is used to form an angle spectrum function from a bit string. For example, $R^{-1}_{xx}$ is transformed into ‘02’.

Chromosomes ‘702’, ‘072’ and ‘027’ also equal ‘02’.

By using the assignment of genes listed in Table 1 and Polish notation, the angle spectrum function of the Capon method $P_{CP}$:

$$P_{CP}(\theta) = \frac{1}{a^H(\theta)R_{xx}a(\theta)}$$

is converted into ‘01302’ through the tree expression shown in Fig. 2. Chromosome ‘561302’ also becomes the angle spectrum function of $P_{CP}$. In the same manner, the angle spectrum function of the beamformer method $P_{BF}$:

$$P_{BF}(\theta) = a^H(\theta)R_{xx}a(\theta)$$

is transformed into ‘513243’.

2.3 Generating Optimum DOA Estimation Algorithm by Using GA

Figure 3 shows the detailed procedure of the proposed method. First, the GA generates first generation chromosomes, which are randomly selected. The number of chromosomes in one generation is called a “population”. Next, chromosomes of the first generation are translated into angle spectrum functions, as described in the previous subsection. Then, DOA estimation simulation is conducted by using each angle spectrum function. The RMSE of each angle spectrum function is used as the fitness value of the chromosome in the GA. The next generation chromosomes are selected from the chromosome of the parent generation whose fitness is better. Through crossover and mutation, next generation chromosomes are then generated. Optimization using the GA is repeated until fitness conditions are satisfied or chromosomes converge. Finally, an optimum chromosome is obtained.

The mechanism of how the proposed method can create a new angle spectrum function is shown in Fig. 4. In this example, chromosomes of the parent generation are ‘513243’ and ‘01302’, which correspond to the angle spectrum functions of $P_{BF}$ and $P_{CP}$. At a crossover stage, the GA randomly selects the crossover point. In this example, this is selected before the second gene. By the crossover, a part of the chromosome is exchanged. This operation means the exchange of the sub-tree in the tree expression. Since this operation is executed symbolically without considering mathematics, the resultant chromosome by crossover may not be calculable due to inconsistency in the number of operands or the size of the matrix. For example, chromosome ‘513202’
in Fig. 4 is not calculable because a matrix comes in denominator. In such a case, fitness of 999 degrees is returned to the GA without conducting DOA estimation simulation.

DOA estimation algorithms are generally classified as spectral-based methods or parametric methods [1]. The range of the proposed method is limited to the spectral-based method. Spectral-based methods are classified as beamforming type or subspace-based types. In the assignment of genes listed in Table 1, the proposed method is limited to the beamforming type. However, by introducing genes that represents a noise subspace matrix, the proposed method can be extended to the subspace-based type.

### Table 2 Parameters of GA.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Length of gene</td>
<td>3 bits</td>
</tr>
<tr>
<td>Length of chromosome</td>
<td>6 genes (18 bits)</td>
</tr>
<tr>
<td>Population size</td>
<td>50</td>
</tr>
<tr>
<td>Crossover rate</td>
<td>0.6</td>
</tr>
<tr>
<td>Mutation rate</td>
<td>0.01</td>
</tr>
<tr>
<td>Total number of trials</td>
<td>10000</td>
</tr>
</tbody>
</table>

### Table 3 Simulation conditions.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Array configuration</td>
<td>Uniform linear array</td>
</tr>
<tr>
<td>Antenna element</td>
<td>isotropic</td>
</tr>
<tr>
<td>Element spacing</td>
<td>Half wavelength</td>
</tr>
<tr>
<td>Number of elements</td>
<td>8</td>
</tr>
<tr>
<td>Number of waves</td>
<td>2 (uncorrelated, equal power)</td>
</tr>
<tr>
<td>Number of snapshots</td>
<td>100</td>
</tr>
<tr>
<td>SNR</td>
<td>20 dB</td>
</tr>
</tbody>
</table>

### Table 4 Radio environment 1.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOA of 1st wave</td>
<td>$\theta_1 = -80 \text{deg. to 65 deg.}$</td>
</tr>
<tr>
<td>DOA of 2nd wave</td>
<td>$\theta_2 = \theta_1 + 15 \text{deg.}$</td>
</tr>
</tbody>
</table>

3. Demonstration

3.1 Creation of New DOA Estimation Algorithm by Using Proposed Method

To validate the effectiveness of the proposed method, we conducted a computer demonstration. Parameters of the GA are listed in Table 2. The array antenna and radio environment conditions are listed in Tables 3 and 4, respectively. In this calculation, the number of incoming waves was assumed to be 2. The average RMSE of each incoming waves was used as the fitness value.

Convergence of the fitness value is shown in Fig. 5. The fitness values show the average RMSE of the corresponding angle spectrum function. A fitness of 999 degrees means that the corresponding chromosomes cannot be converted to angle spectrum functions due to the inconsistency of operators and operands at the Polish notation stage. A fitness value around 90 degrees means that the corresponding chromosomes are successfully converted to the angle spectrum function, but they do not act as a DOA estimation algorithm.
A fitness value under 1 degree means that the corresponding chromosomes are converted to angle spectrum functions and successfully act as a DOA estimation algorithm. After 5000 trials, chromosomes were converged.

The chromosomes that gave the top 5 fitness values are listed in Table 5. The angle spectrum function \( P_{OPT} \) that corresponds to the chromosome with the best fitness value is

\[
P_{OPT}(\theta) = \frac{1}{\mathbf{a}^H(\theta) \mathbf{R}_{xx} \mathbf{a}(\theta)}.
\]  

(3)

The second-best algorithm was the Capon method. From this result, the proposed method can create a new angle spectrum function.

### 3.2 Validation of Created DOA Estimation Algorithm

At first, we evaluated the angle spectrum function under the same conditions listed in Table 3. In this calculation, the radio environment conditions are listed in Table 6. The angle spectrum functions are shown in Fig. 6. We found that the \( P_{OPT} \) has the sharpest angle spectrum.

Next, we examined the performance of the \( P_{OPT} \) under the simulation and radio environment conditions listed in Tables 3 and 4. The performance was evaluated using RMSE calculated through 100 independent trials. The results are shown in Fig. 7, which also shows the Cramer-Rao bound (CRB) [10]. We found that the \( P_{OPT} \) has the best RMSE for the endfire direction. This is because the angle spectrum becomes broader for the endfire direction, thus the sharp spectrum of the \( P_{OPT} \) is effective. On the other hand, RMSE of the \( P_{OPT} \) for the broadside direction is as same as the Capon method. This is because the peak direction of the angle spectrum is unchanged although the angle spectrum of the \( P_{OPT} \) becomes sharper than the Capon method.

For several incoming waves, the resolution of DOA estimation is also an important index. Figure 8 shows the resolution, which is defined by the angle separation at which the peak of the spectrum function is split into two peaks when the separation of two incoming waves increased from 0 degrees. We found that \( P_{OPT} \) has the best resolution for all directions. This is because the \( P_{OPT} \) has the sharpest angle spectrum.

### 4. Conclusion

We proposed a method for automating the trial-and-error creation of DOA estimation algorithms by using a GA. Through computer simulation, we found that the proposed method can create a new angle spectrum function. The created angle spectrum function has better resolution than the Capon method.

In antenna design, simulator- and optimizer-based automated design is now commonly used. It is expected that the proposed method will become a beneficial tool in DOA estimation.
estimation algorithm design.

For future work, we will introduce a gene that represents a noise subspace matrix to extend the proposed method to a subspaced-based DOA estimation algorithm.

Acknowledgment

This work was partially supported by KAKENHI for Young Scientists (B) 22760274.

References